

**OL-015 Vaccine challenge studies by passively immunizing poultry birds with H7N3 polypeptide specific antisera against lethal dose of H7N3**

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This study was aimed at developing a vaccination strategy that could provide protection against highly pathogenic avian influenza virus (AIV), H7N3 and its variants outbreaks. A purified viral stock of highly pathogenic H7N3 isolate was lysed to isolate viral proteins by electrophoresing on 12% sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), followed by their elution from gel through trituration in phosphate buffered saline (PBS). Overall, five isolated viral polypeptides/proteins upon characterization were used to prepare hyperimmune monovalent serum against respective polypeptides independently and a mixture of all five in poultry birds, and specificity confirmation of each antiserum through dot blot and Western blotting. Antiserum generated from various group birds was pooled and evaluated in 2-week old broiler chicken, for its protection against viral challenge. To evaluate in-vivo protection of each antiserum against viral challenges, six groups of 2-week old broiler chicken were injected with antiserum and a seventh control group received normal saline. Each group was exposed to purified highly pathogenic AIV H7N3 strain at a dose 10<sup>5</sup> embryo lethal dose (ELD<sub>50</sub>). We observed that nucleoprotein (NP) antiserum significantly protected birds from viral infection induced morbidity, mortality and lowered viral shedding compared with antiserum from individual viral proteins or mixed polypeptides/proteins inclusive of NP component. The capability of individual viral polypeptide specific antisera to protect against viral challenges in decreasing order was nucleoprotein (NP) > hemagglutinin (HA) > neuraminidase (NA) > viral proteins mix > viral polymerase (PM) > nonstructural proteins (NS). Our data provide proof of concept for potential utilization of passive immunization in protecting poultry industry during infection outbreaks. Furthermore conserved nature of avian NP makes it an ideal candidate to produce antiserum protective against viral infection.

**Free Paper Presentation 4: Respiratory Tract/Bacterial Infections**

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**PL-004 Viral and *Mycoplasma pneumoniae* community acquired pneumonia and novel clinical outcome evaluation in ambulatory adult patients**

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**Background:** Few studies have addressed the etiology and clinical outcomes associated with antimicrobial regimens of CAP treated in an ambulatory setting.

**Methods:** Culture of *Mycoplasma pneumoniae* as well as urine for rapid antigen testing of *Streptococcus pneumoniae*

and *Legionella pneumoniae* were obtained. Presence of 8 kinds of respiratory virus DNA or RNA from respiratory secretion were determined. Treatment outcomes were measured by speed of resolution of morbidities.

**Results:** 197 patients were enrolled in the study, with the median age of 32.5 years. Overall an etiological diagnosis was made in 51.8% of the patients. The most common pathogens were *M. pneumoniae* (29.4%) followed by Influenza virus A, parainfluenza virus, adenovirus, human metapneumovirus (9.6%) and *Streptococcus pneumoniae* (4.1%). Patients with mycoplasma infections were younger and less likely to present with purulent sputum. Among patients infected with *M. pneumoniae*, those with quinolones as initial prescriptions had shorter duration of fever after initiation of antibiotics than patients with  $\beta$ -lactams, macrolides, or  $\beta$ -lactam + macrolides ( $p < 0.05$ ).

**Conclusions:** *M. pneumoniae* and respiratory viruses (Influenza A, parainfluenzae, adenovirus, human metapneumovirus) were the most frequent pathogens found in ambulatory adult CAP patients; quinolones were better than  $\beta$ -lactams, macrolides, or  $\beta$ -lactam + macrolides in resolution of fever of *M. pneumoniae* pneumonia.

**OL-016 Epidemiology study of community-acquired pneumonia in different age groups**

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**Background and Aim:** Despite of the detailed study of community-acquired pneumonia, the role of atypical microorganisms such as *M. pneumoniae*, *C. pneumoniae* and *L. pneumophila* is not still defined. Also there are some discussions about role of the associations of these bacteria with the other so-called typical microorganisms as *S. pneumoniae* and *H. influenzae* as well as the place of the viral pathogens in community-acquired pneumonia etiology structure. The aim of our research was to define the etiology of the community-acquired pneumoniae in young adults (17–34 years, 1st group) and to compare the results with the data gained in aged patients (<60 years, 2nd group).

**Methods:** The 300 young and 300 aged patients with community-acquired pneumonia were screened with bacteriological, disk-diffusion with MIC, PCR and other methods.

**Results:** Bacterial associations were defined in 55% versus 72% in 2<sup>nd</sup> group. *M. pneumoniae* was identified in 39% vs 19%, *C. pneumoniae* 33.4% vs 24%. The bacterial pathogens were represented with the species *S. pneumoniae* (58.44%/42%), *H. influenzae* (15.06%/21%), *M. catarrhalis* (26.23%/7%). Among the viral pathogens the most often was metapneumovirus in young adults (23%), and influenzae virus in aged patients (18%). The most prevalence bacteria were genotyped and there were revealed the relations between several isolates of *M. pneumoniae* and *S. pneumoniae* existing as association in several cases of different age groups what proved the epidemiological character of the spread of this association.

**Conclusion:** Some changes in etiology structure of community-acquired pneumonia seems to be connected with the changes in immunology peculiarities of different age groups, as well as with the other epidemiology reasons. **Acknowledgment:** Research project was supported by the President Grant for the Candidate of Science (MK-2795.2008.7).